

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/553,386
Source: 11FWP
Date Processed by STIC: 11/11/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/553 386

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleis
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION for SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (See item 11 below)
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,386

DATE: 01/11/2007

TIME: 09:47:27

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01112007\J553386.raw

Does Not Comply
Corrected Diskette Needed

see item 4 on
Error Summary Sheet

2 <110> APPLICANT: Hallenbeck, Paul
3 Hampton, Garret
4 Hay, Carl
5 Huang, Ying
6 Jakubczak, John
W--> 7 <120> TITLE OF INVENTION: TMRSS2 REGULATORY SEQUENCES AND USES THEREOF
W--> 8 <130> FILE REFERENCE: 3802-166-27 NATL
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/553,386
C--> 9 <141> CURRENT FILING DATE: 2005-10-17
9 <150> PRIOR APPLICATION NUMBER: 10/553,386
11 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: FastSeq for Windows Version 4.0

delete - this is not a prior application
number

ERRORRED SEQUENCES

W--> 13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1811
15 <212> TYPE: DNA
16 <213> ORGANISM: H. sapiens
W--> 17 <400> SEQUENCE: 1
18 agagcttccc aggaaggagg cagtgaagca aggcagcctg ggaatggggct 60
19 tttttctgct tccacctcat tttaaagcaa atcatgttga tttgtatat atgcagggga 120
20 ggagaaaaca tgcttcccct ctacccttct agttcgttca gctagtctac aaattaaatt 180
21 ggcatacaat agatgaacag gagaaaagct gtttaaatgt atgtactcac agatgggaat 240
22 ccacacaagaa tatgagactt aaagaacagc ccagggtgagt gaggggtcca gtgcgggggc 300
23 tcacacctgt aatcccagca ctttgggagg ccaaggcagg tggatcgctt gagcccatg 360
24 tggagaccag tctgggtaac ataggggagac ccccatctct acaaaaaatt aaattagctg 420
25 ggcgtggttg cacacgcctc tagtcccagc tactcgggag gctgaggttg gaggattact 480
26 tgtgccttgg gaggttgaag ctgccatgag ccattgattga gccactgcac tccaaccttg 540
27 gcaacagagt gagacccttt ctgggggaaa aaaaaacaca cgaaaaaaa aaggtgcagc 600
28 agcccgatga ttgaggctta tctgtcactc tgagtgcagc aaagaaatgg gggtttgagg 660
29 ctctctggga gcggtggagg agtgagggga ccgtgaggag aggaggtgtc tggtaaacgc 720
30 aggttgcctg gtgaggcaga taaaagtctc ccagggtgata aaagtgtctc ggaacacgtc 780
31 ctcttctctg tacagatctg ctgactaaca aacatttctt ttatagggtc aaatttctct 840
32 tacaaaaggc cattttctca gaggtactct ggtgtctgca gttcctcaac ataaccagtt 900
33 ccaaatcatc aatgtgccaa agaggactat gttggggtag cagattcttg tctcctccag 960
34 tctacttggg ggtgatgaat tctgtcttac ggtcctatta aattctggtg aattctgagt 1020
35 ccccaacaatt gcaaacatta gaaagaacct ctcaagtgcc cgggaacagc cagctcttcc 1080
E--> 36 tggctgaggt gtgttgcacc acttctctac tcccgccctg gccggtggtg ccgagagacc 1140
37 tggggaccatc cgggggagcc ctttccaccg gacgctggtg ggggccaaga aatgccagcc 1200
38 tagggggagt ggggaggggtc ttggcgctcc ggcgctgtgt cccgcacact cgtgcttggtg 1260
E--> 39 ccagcagctc ccaaggccta ctgtgggtc cttgccacga ggctacagtg ggttccccgg 1320

inhibits nucleic
acid
designator

see p. 2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/553,386

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01112007\J553386.raw

40 aggccaaagac ggggcccggcc gcctacagga gctcgtgagg tagcagctcc gggggctcac 1380
41 ccaggactcc aggagcgctc ccagaaatcc ccttccttaa cccaaactcg agccctcggg 1440
E--> 42 cagcgctcgc ccgcccggcag gagaggggca ggttgggcgc tgtggccggg cccgggaagc 1500 *invalid*
43 gccccagagt cccttatggg tccctccgca gccgggggtg agccaggcag ggaaccgcgc 1560
44 cggacttccc ttgggaaacg cctcctcccg ccgccccgc ccccgccccgc ccagggtgac 1620
45 ccgcgaccgc cttgggggtg tcgccctgga ccctgggaca ccgcctcctg agattaaagc 1680
46 gagagccagc gcgggcccgg ccgagtaggc gcgagctaag caggaggcgc aggcggaggc 1740
47 ggagggcgag gggcggggag cgccgcctgg agcgcggcag gtgagcggcg ccggtaccag 1800
48 ggtcccggct c 1811

49 <210> SEQ ID NO: 2

50 <211> LENGTH: 239

51 <212> TYPE: DNA

52 <213> ORGANISM: H. sapiens

56 <400> SEQUENCE: 2

57 cgtggcggag ggactgggga ccggggcacc cgtcctgccc cttcaccttc cagctccgcc 60

58 tcctccgcgc ggaccgcgc ccgtcccgc cctcccccgg tccccggccc agccccctcc 120

59 gggccctccc agccccctcc cttcctttcc gcggccccgc cctctcctcg cggcgcgagt 180

E--> 60 ttcaggagc gctgcgtcct gctgcgcacg tgggaagccc tggccccggc cccccccc 239

95 <210> SEQ ID NO: 8

96 <211> LENGTH: 270

97 <212> TYPE: DNA

98 <213> ORGANISM: H. sapiens

W--> 99 <400> SEQUENCE: 8

100 tggtagccatc cggacaaagc ctgcgcgcgc ccgccccgc cattggcgt accgccccgc 60

101 gccgcccgc catcccgccc ctgcgcgcgc ggtccggcgc gttaaagcca ataggaaaccg 120

102 ccgcggtgt tcccgccacg gccggggcag ccaattgtgg cggcgctcgg cggtcgtgg 180

103 ctctttccgc gcaaaaagga tttggcgcgt aaaagtggcc gggactttgc aggcagcggc 240

104 ggccgggggc ggagcgggat cgagccctcg 270

E--> 110 sanF1\359709.1

E--> 112 - 1 - *delete*

VERIFICATION SUMMARY DATE: 01/11/2007
PATENT APPLICATION: US/10/553,386 TIME: 09:47:28

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\01112007\J553386.raw

L:7 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:283 W: Missing Blank Line separator, <210> field identifier
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:39 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:42 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:60 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:65 M:283 W: Missing Blank Line separator, <400> field identifier
L:75 M:283 W: Missing Blank Line separator, <400> field identifier
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:110 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:110 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:276 SEQ:8
L:110 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:110 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=8
L:112 M:252 E: No. of Seq. differs, <211> LENGTH:Input:270 Found:276 SEQ:8